

FIGURE 1a
FIGURE 1b
FIGURE 1c
FIGURE 1d
FIGURE 1e

10 20 30 40 50 60
phyA-1. seq: ATGGGAAGAAATTGCTAGAGGCTCAAAAAATGAGTTCTCTCATTTGTGCTTTGCTGTAGTA
|||||
phyA-2. seq: ATGGGAAGAAATTGCTAGAGGCTCAAAAAATGAGTTCTCTCATTTGTGCTTTGCTGTAGTA
|||||

70 80 90 100 110 120
phyA-1. seq: TTGGTGTCACCTCAATTTGGCTTCCGAAACACACAGCTGCCATGCTGGCAGTCCCCGCCCTCG
|||||
phyA-2. seq: TTGGTGTCACCTCAATTTGGCTTCCGAAACACACAGCTGCCATGCTGGCAGTCCCCGCCCTCG
|||||

130 140 150 160 170 180
phyA-1. seq: AGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAATGCTTCTCCGAGACTTCG
|||||
phyA-2. seq: AGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAATGCTTCTCCGAGACTTCG
|||||

190 200 210 220 230 240
phyA-1. seq: CATCTTTGGGGTCAATACGCACCGTTCTTCTCTCTGGCAAACGAATCGGTCACTCCCCCT
|||||
phyA-2. seq: CATCTTTGGGGTCAATACGCACCGTTCTTCTCTCTGGCAAACGAATCGGTCACTCCCCCT
|||||

250 260 270 280 290 300
phyA-1. seq: GAGTGCCCGCGGATGCAGAGTCACTTTCGCTCAGGTCTCTCCCCGTATGGAGCGCG
|||||
phyA-2. seq: GATGTTCTGCGGATGCCATGTCACTTTCGCCCAGGTTCTCTCCCCGTATGGAGCACGG
|||||

FIGURE 1a

FIGURE 1b

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610 620 630 640 650 660
phyA-1. seq: CGTGCCAGCCCGGCCAATCGTCGCCCAAGATCGACGTGGTCAATTCGAGGCCAGCTCA
|||||
phyA-2. seq: CGTGCCAGCCCGGCCAATCGTCGCCCAAGATCGACGTGGTCAATTCAGAGGCCAGCAC
670 680 690 700 710 720
phyA-1. seq: TCCAACAACACTCTCGACCCAGGCACCTGCACGTGTCTTCGAAGACAGCGAATTGGCCGAT
|||||
phyA-2. seq: TCCAACAACACTCTCGATCCGGGCACCTGCACCGTTTTCGAAGATAGCGAATTGGCCGAT
730 740 750 760 770 780
phyA-1. seq: ACCGTCGAAGCCCAATTTCACCGCCACGTTTCGTCCCTCCATTTCGTCAACGCTGGAGAAC
|
phyA-2. seq: GACATCGAAGCCCAATTTCACCGCCACGTTTCGTCCCTCCATTTCGTCAACGCTGGAGAAT
790 800 810 820 830 840
phyA-1. seq: GACCTGTCCGGTGTGACTCTCACAGACACAGAAAGTGACCTACCTCATGGACATGTGCTCC
|||
phyA-2. seq: GACTTGTCTGGCGTGTCTCTCACGGACACAGAAAGTGACCTACCTCATGGACATGTGCTCC
850 860 870 880 890 900
phyA-1. seq: TTCGACACCATCTCCACCAAGCACCGTCGACACCAAGCTGTCCCCCTTCTGTGACCTGTTT
|||||
phyA-2. seq: TTCGACACCATCTCCACCAAGCACCGTCGACACCAAGCTGTCCCCCTTCTGTGACCTGTTT

FIGURE 1c

	910	920	930	940	950	960
phyA-1. seq:	ACCCATGACGAATGGATCAACTACGACTACCTCCAGTCCCTTGAAAAAGTATTACGGCCAT					
phyA-2. seq:	ACCCATGAAGAATGGATCAACTACGACTACCTCCAGTCCCCGAAACAAATACTACGGCCAT					
	970	980	990	1000	1010	1020
phyA-1. seq:	GGTGCAGGTAACCCGCTCGGCCCGACCCAGGGCGTGGCTACGCTAACGAGCTCATCGCC					
phyA-2. seq:	GGCGCAGGTAACCCGCTCGGCCCGACCCAGGGCGTGGCTACGCTAACGAGCTCATCGCC					
	1030	1040	1050	1060	1070	1080
phyA-1. seq:	CGTCTGACCCCACTCGCCTGTCCACGATGACACCAGTTCCAACCACTTTGGACTCGAGC					
phyA-2. seq:	CGTCTCACCCCACTCGCCTGTCCACGATGACACCAGTCCAACCACTTGGACTCCAAC					
	1090	1100	1110	1120	1130	1140
phyA-1. seq:	CCGGCTACCTTTCGGCTCAACTCTACTCTCTACGGGACTTTTCGCATGACAAACGGCATC					
phyA-2. seq:	CCGGCTACTTTCGGCTCAACTCCACTCTCTATGCGGACTTTTCGCATGATAACGGCATC					
	1150	1160	1170	1180	1190	1200
phyA-1. seq:	ATCTCCATTCTCTTTGCTTTAGGTCTGTACAACGGCACTAAGCCGCTATCTACACGACC					
phyA-2. seq:	ATCTCTATCCTCTTTGCTTTGGGTCTGTACAACGGCACCAAGCCGCTGTCTTCCACGACC					

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FIGURE 1e

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FIGURE 2a

FIGURE 2b

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phyA-1.pro: 10 20 30 40 50
MGRIARGSKMSSLIVSLVVLVSLNLASETTAAMLAVPASRNQSSCDTVD
|||||
phyA-2.pro: 60 70 80 90 100
MGRIARGSKMSSLIVSLVVLVSLNLASETTAAMLAVPASRNQSTCDTVD
|||||

phyA-1.pro: 60 70 80 90 100
QGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGAR
|||||
phyA-2.pro: 60 70 80 90 100
QGYQCFSETSHLWGQYAPFFSLANKSAISPDVPAGCHVTFAQVLSRHGAR
|||||

phyA-1.pro: 110 120 130 140 150
YPTDSKGKKYSALIEEIQONATTFDGKYAFLKTYNYSLGADDLTPEGEQE
|||||
phyA-2.pro: 110 120 130 140 150
YPTDSKGKKYSALIEEIQONATTFEGKYAFLKTYNYSLGADDLTPEGEQE
|||||

phyA-1.pro: 160 170 180 190 200
LVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDP
|||||
phyA-2.pro: 160 170 180 190 200
LVNSGVKFYQRYESLTRNIVPFIRSSGSSNRVIAAGNKKFIEGFQSTKLKDP
|||||

phyA-1.pro: 210 220 230 240 250
RAQPGQSSPKIDVVISSEASSNNNTLDPGTCTVFEDSELADTVEANFTATF
|||||
phyA-2.pro: 210 220 230 240 250
RAQPGQSSPKIDVVISSEASTSNNNTLDPGTCTVFEDSELADDDIEANFTATF
|||||

FIGURE 2a

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260 270 280 290 300
phyA-1.pro: VPSIRQRLNDLSGVTLTDTEVTYLMDCSFDTISTSTVDTKLSPFCDLF
|||||
phyA-2.pro: VPSIRQRLNDLSGVSLTDTEVTYLMDCSFDTISTSTVDTKLSPFCDLF
|||||
310 320 330 340 350
phyA-1.pro: THDEWINYDYLSQLKKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDD
||
phyA-2.pro: THEEWINYDYLSQSPNKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDD
|||||
360 370 380 390 400
phyA-1.pro: TSSNHTLDSSPATFPLNSTLYADFSDNGIISILFALGLYNGTKPLSTTT
|||||
phyA-2.pro: TSSNHTLDSNPATFPLNSTLYADFSDNGIISILFALGLYNGTKPLSSTT
|||||
410 420 430 440 450
phyA-1.pro: VENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP LVRVLVNDRVVPLHG
|||||
phyA-2.pro: AENITQTDGFSSAWTVPFASRMVYVEMMQCQSEQEP LVRVLVNDRVVPLHG
|||||
460 470 480
phyA-1.pro: CPVDALGRCTRDSFVRGLSFARSGGDWAECFA
|||||
phyA-2.pro: CPVDALGRCTRDSFVKGLSFARSGGDWAECFA
|||||

FIGURE 2b

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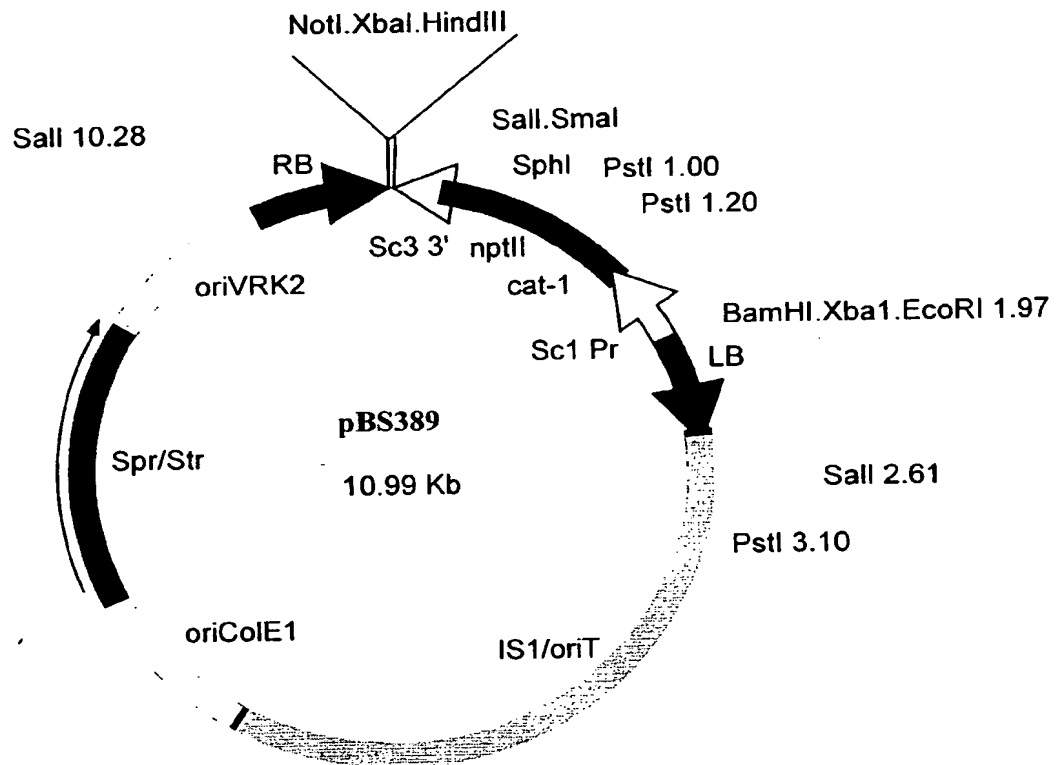


FIGURE 3

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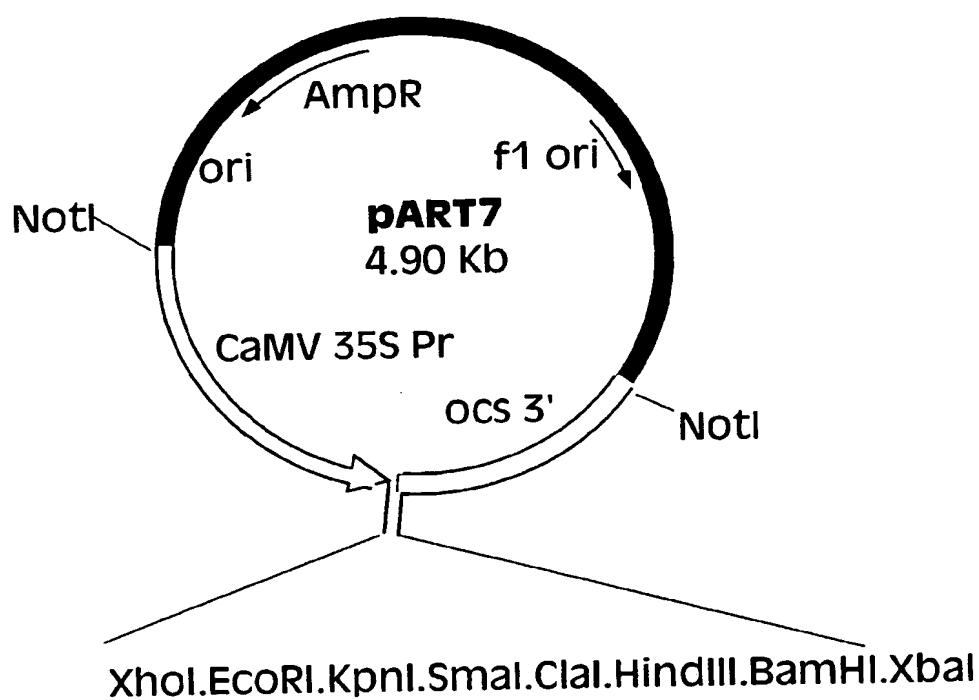


FIGURE 4

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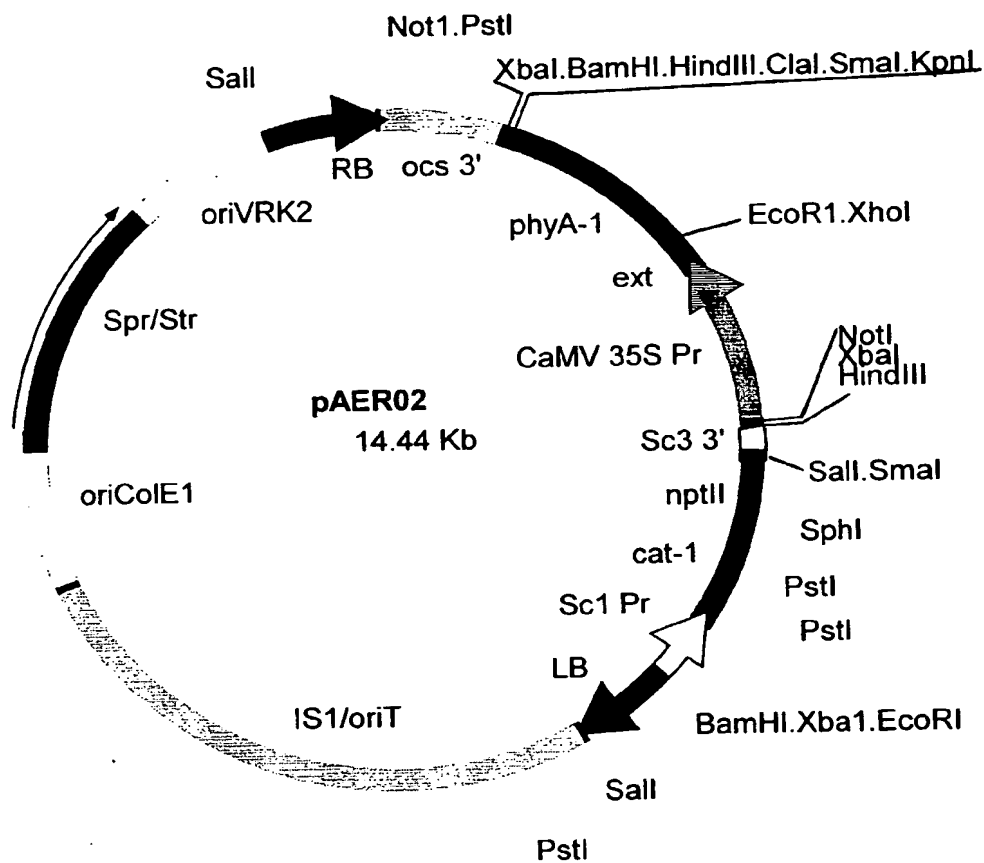


FIGURE 5

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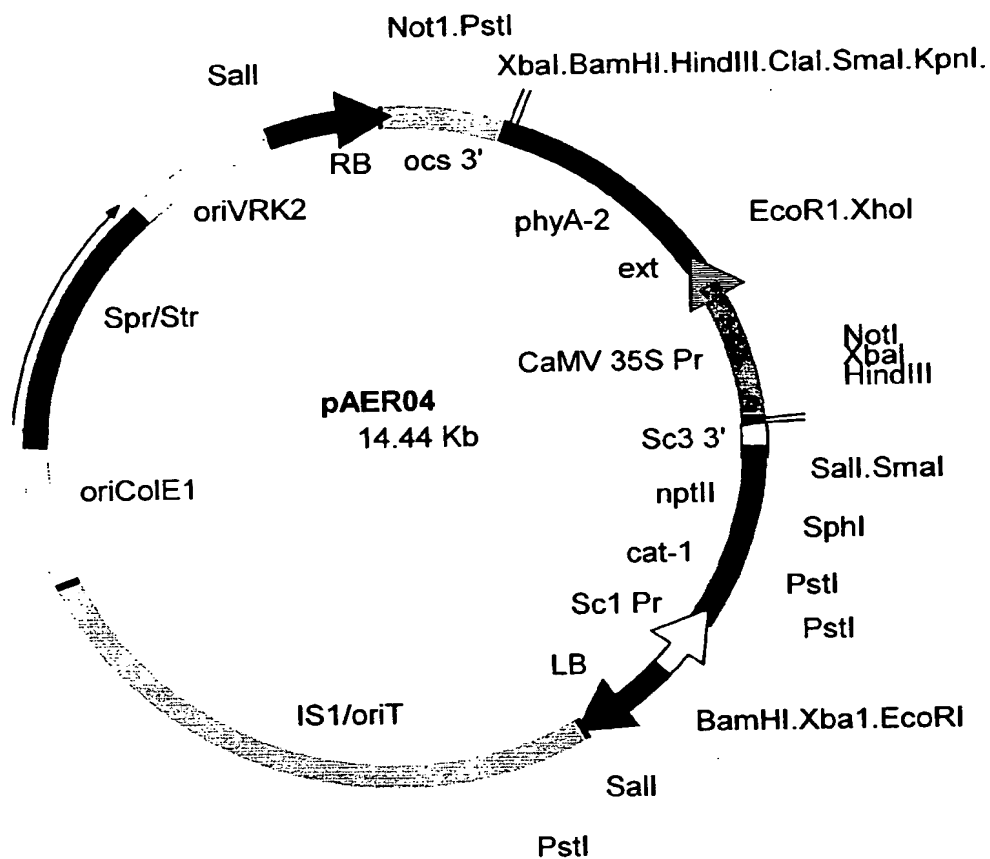


FIGURE 6

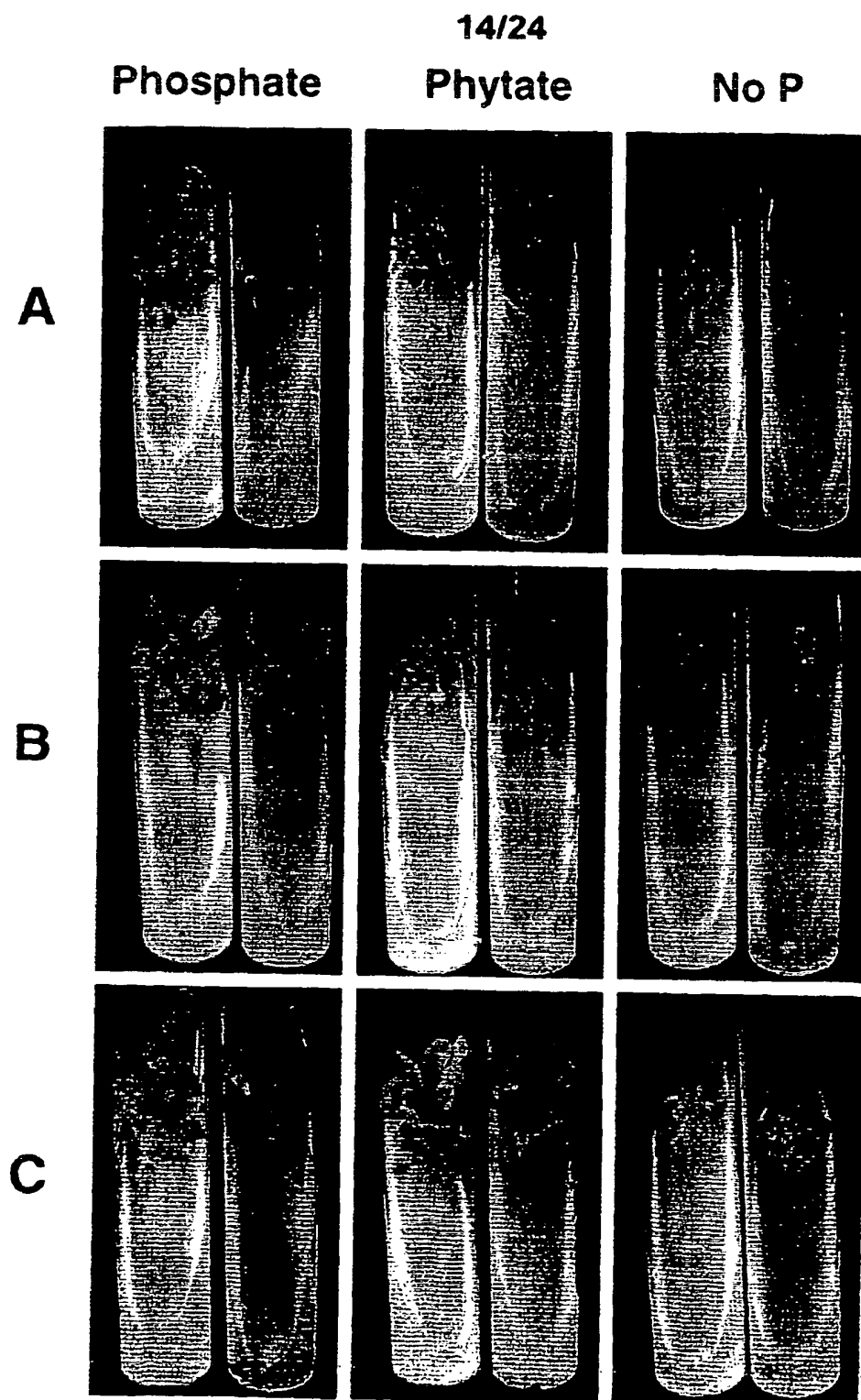


FIGURE 7

Plants supplied with phytate

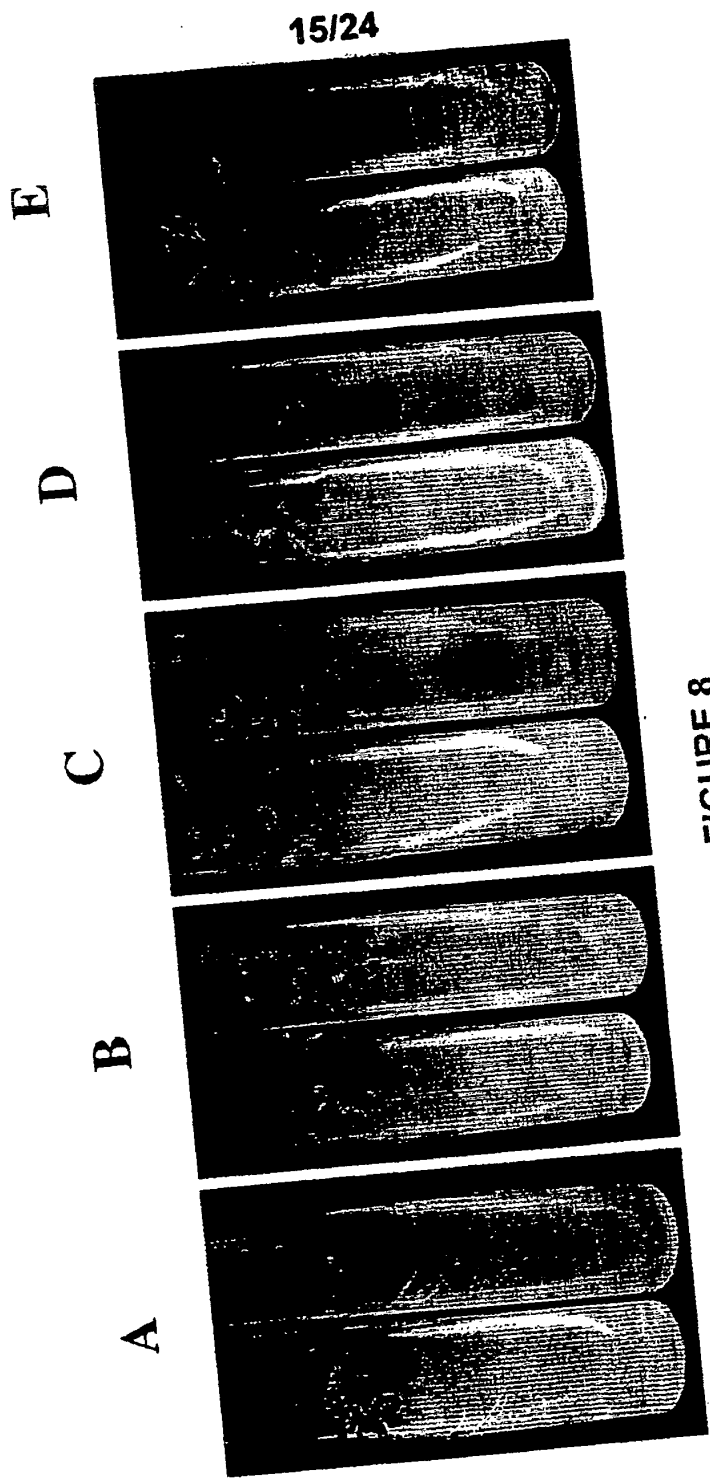


FIGURE 8

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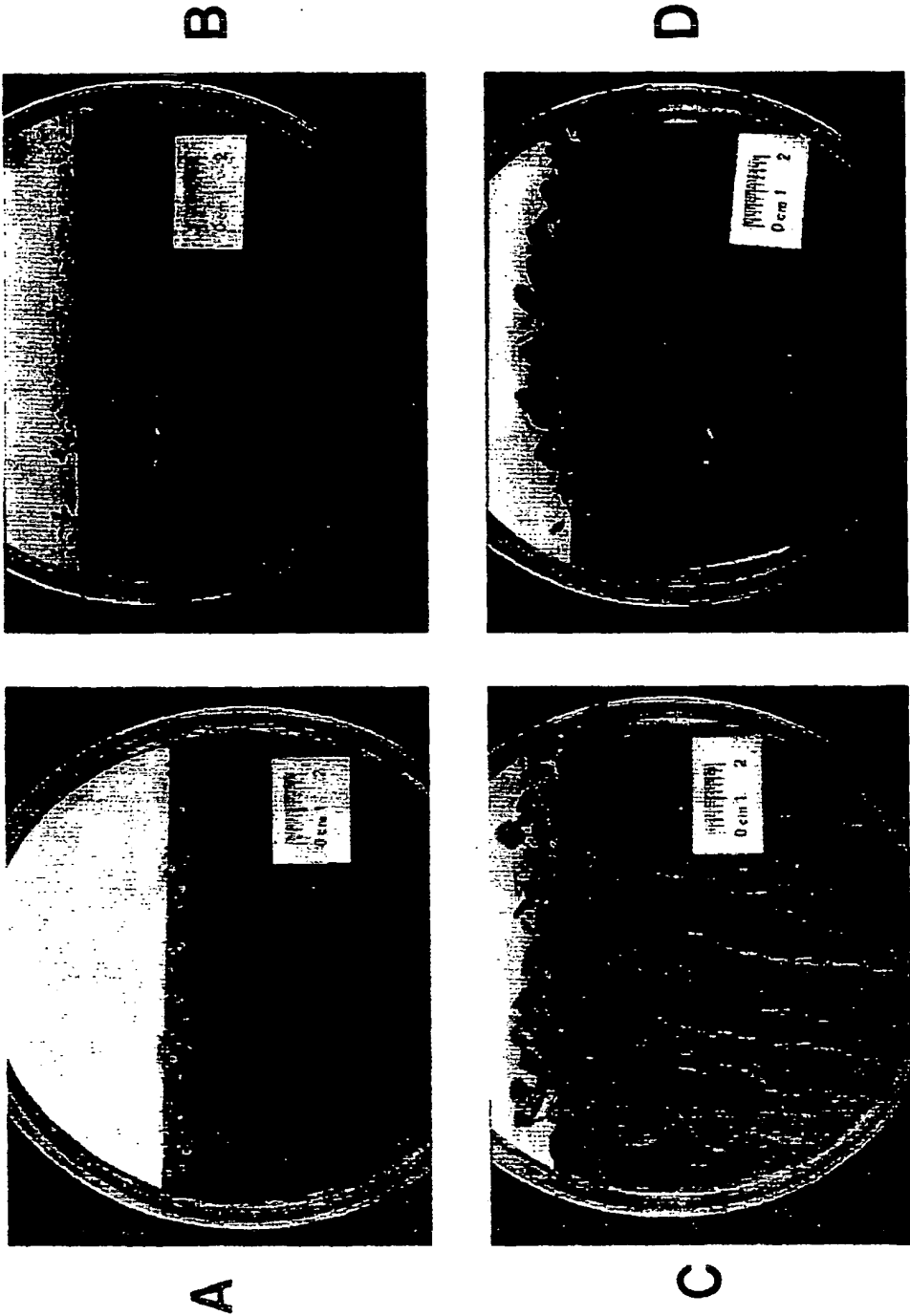
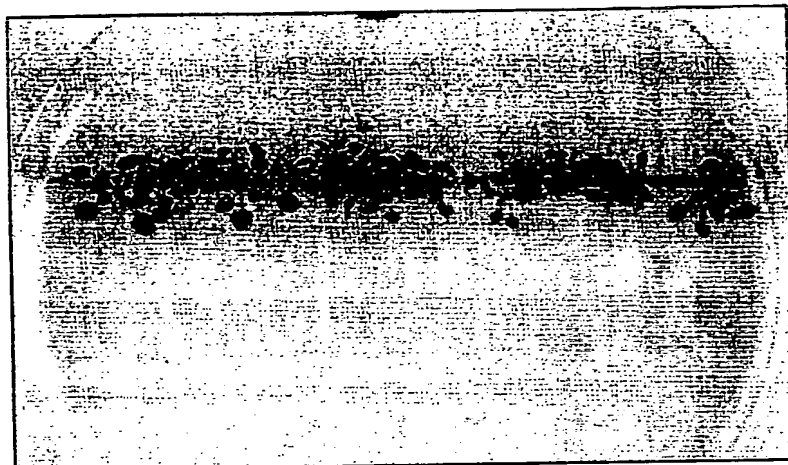


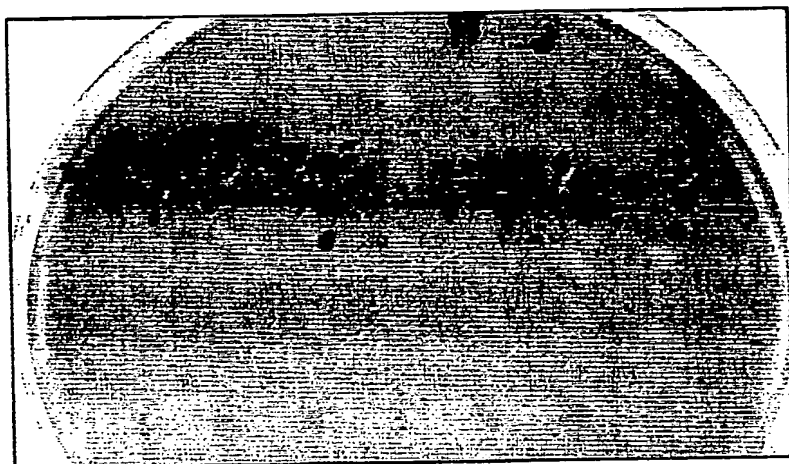
FIGURE 9

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A



B



C

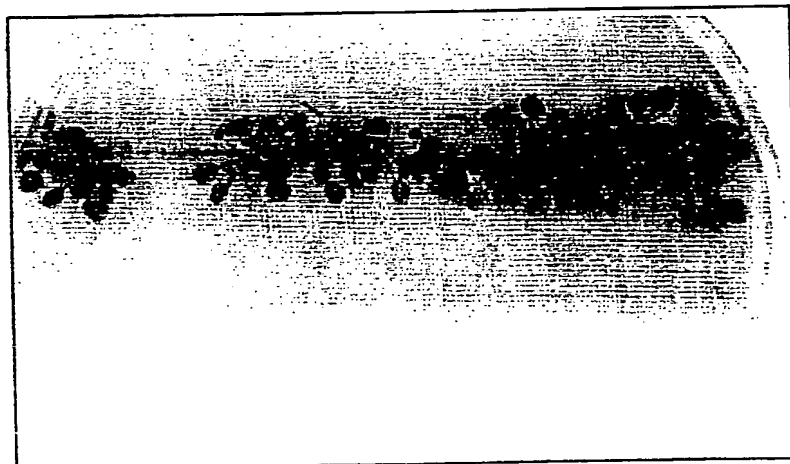
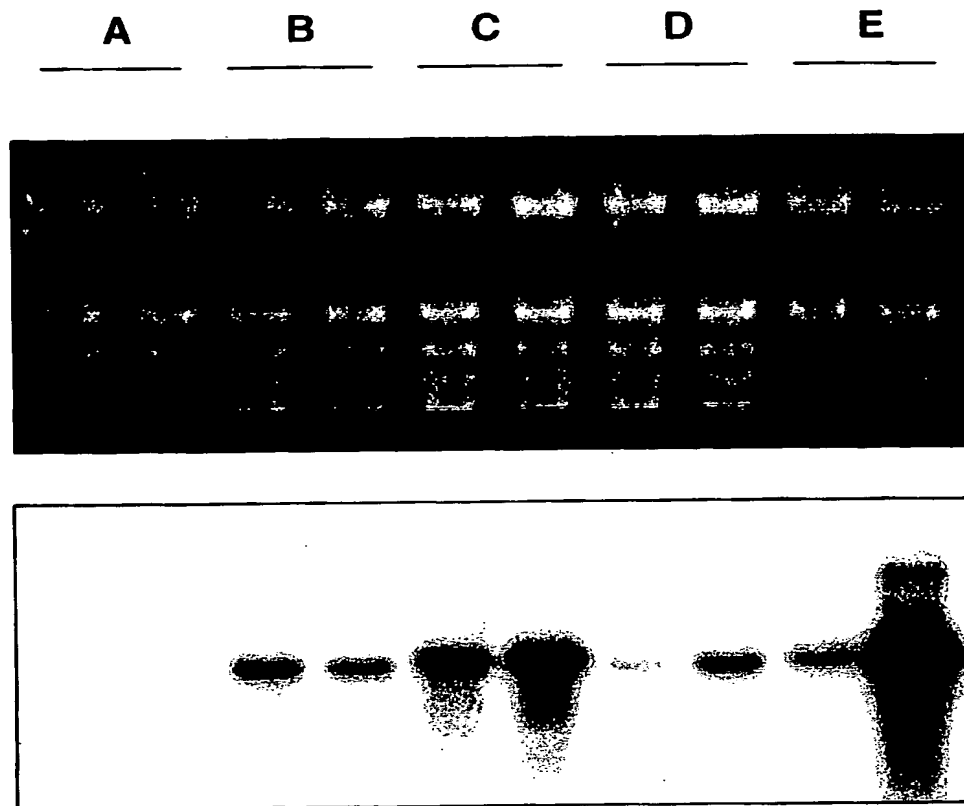


FIGURE 10

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Transgenic *Arabidopsis***FIGURE 11**

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Transgenic *Arabidopsis*

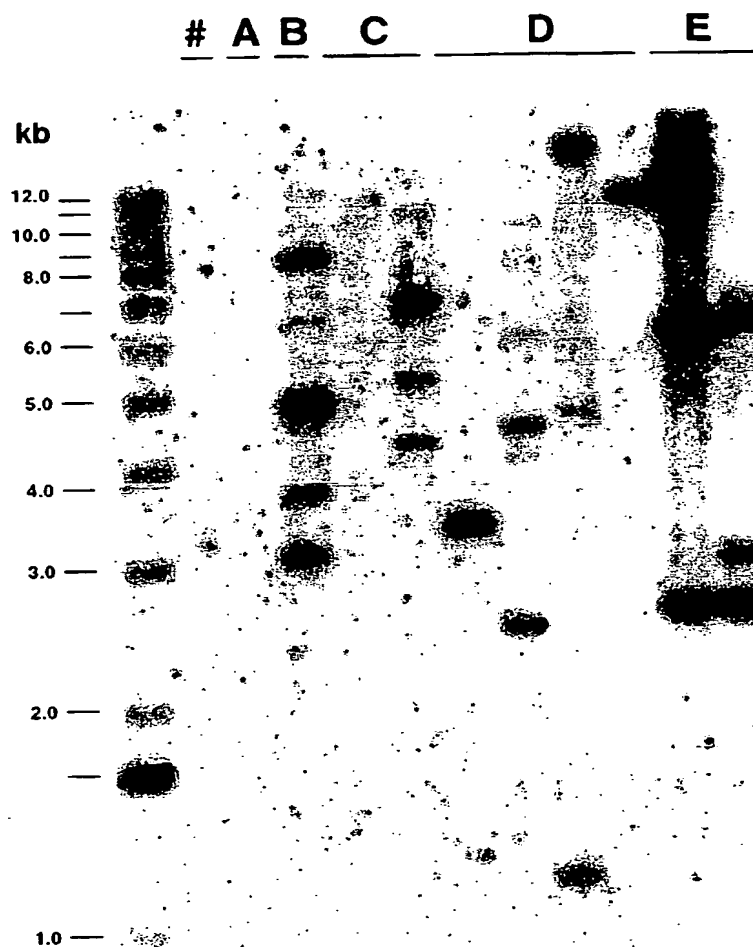


FIGURE 12

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Transgenic subterranean clover

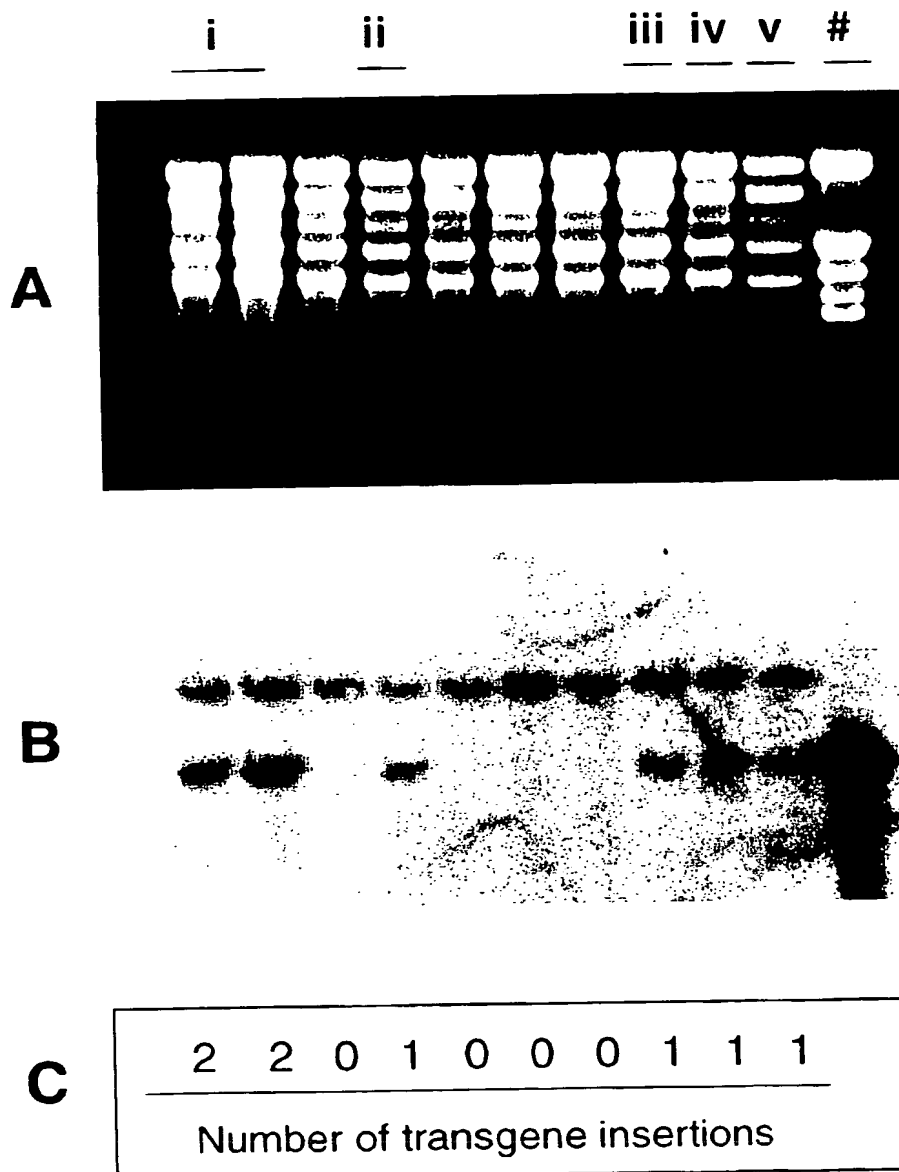


FIGURE 13

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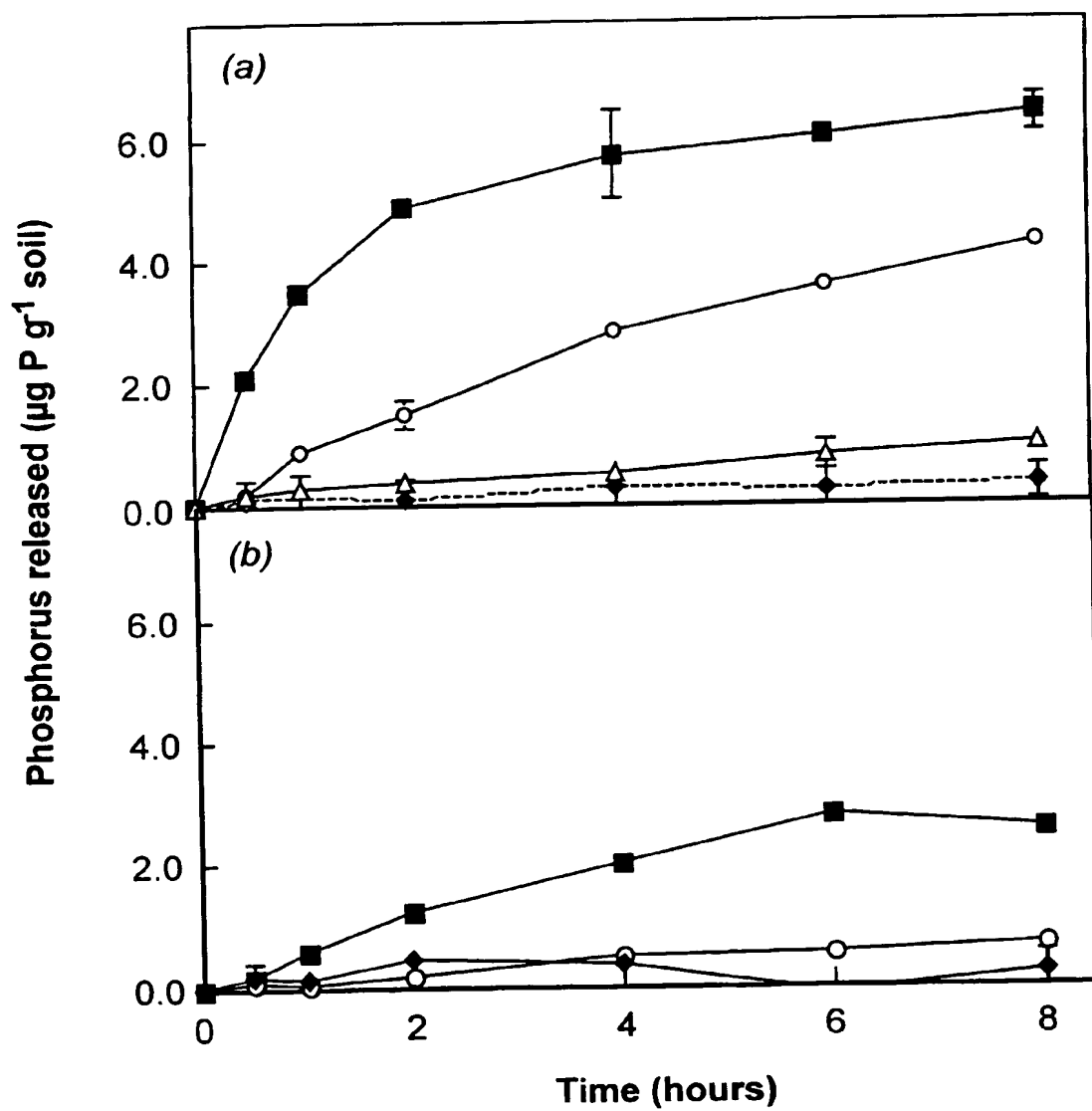


FIGURE 14

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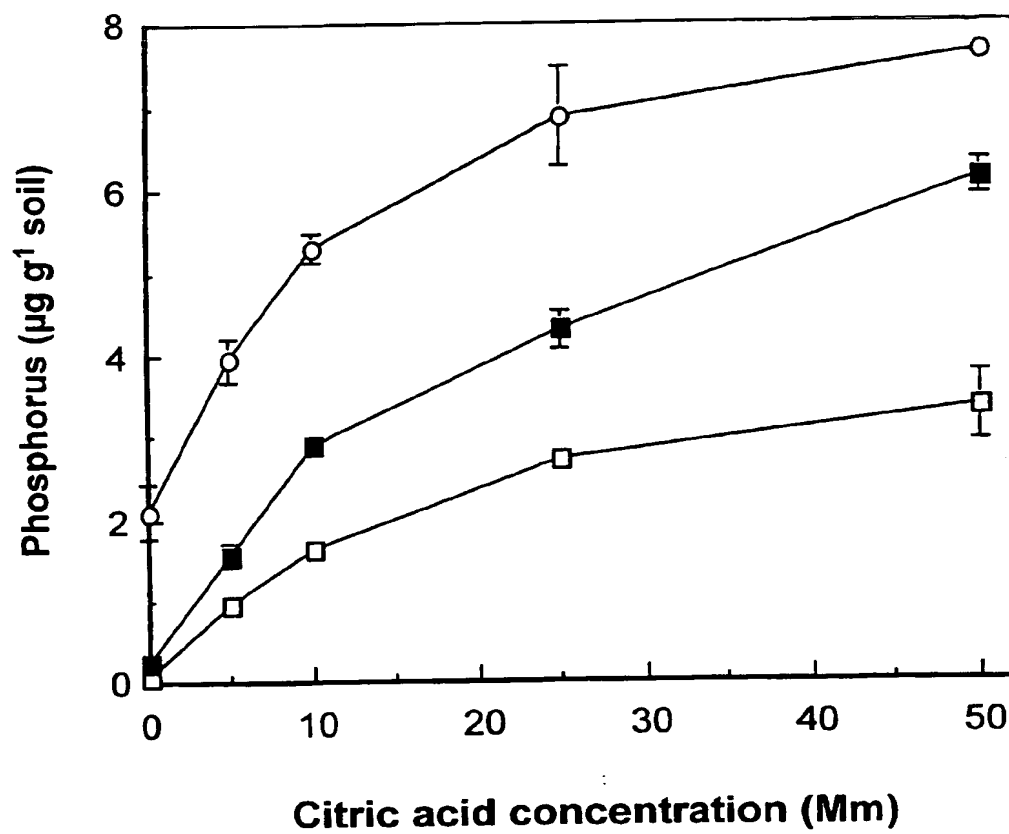


FIGURE 15

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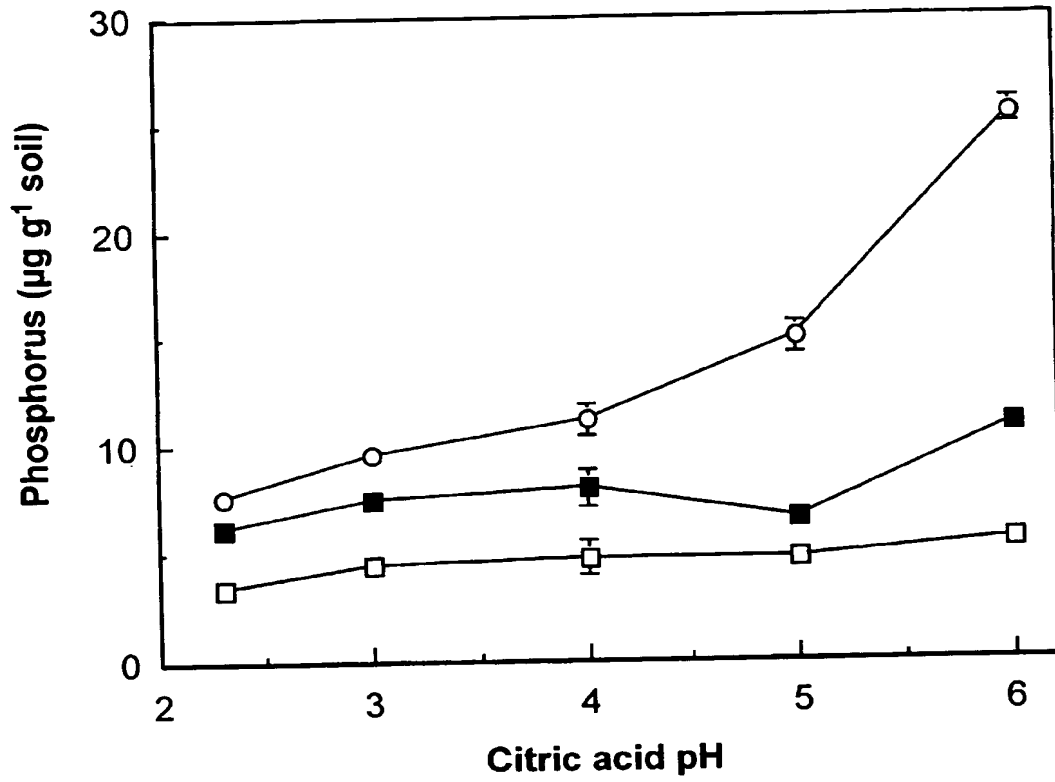


FIGURE 16

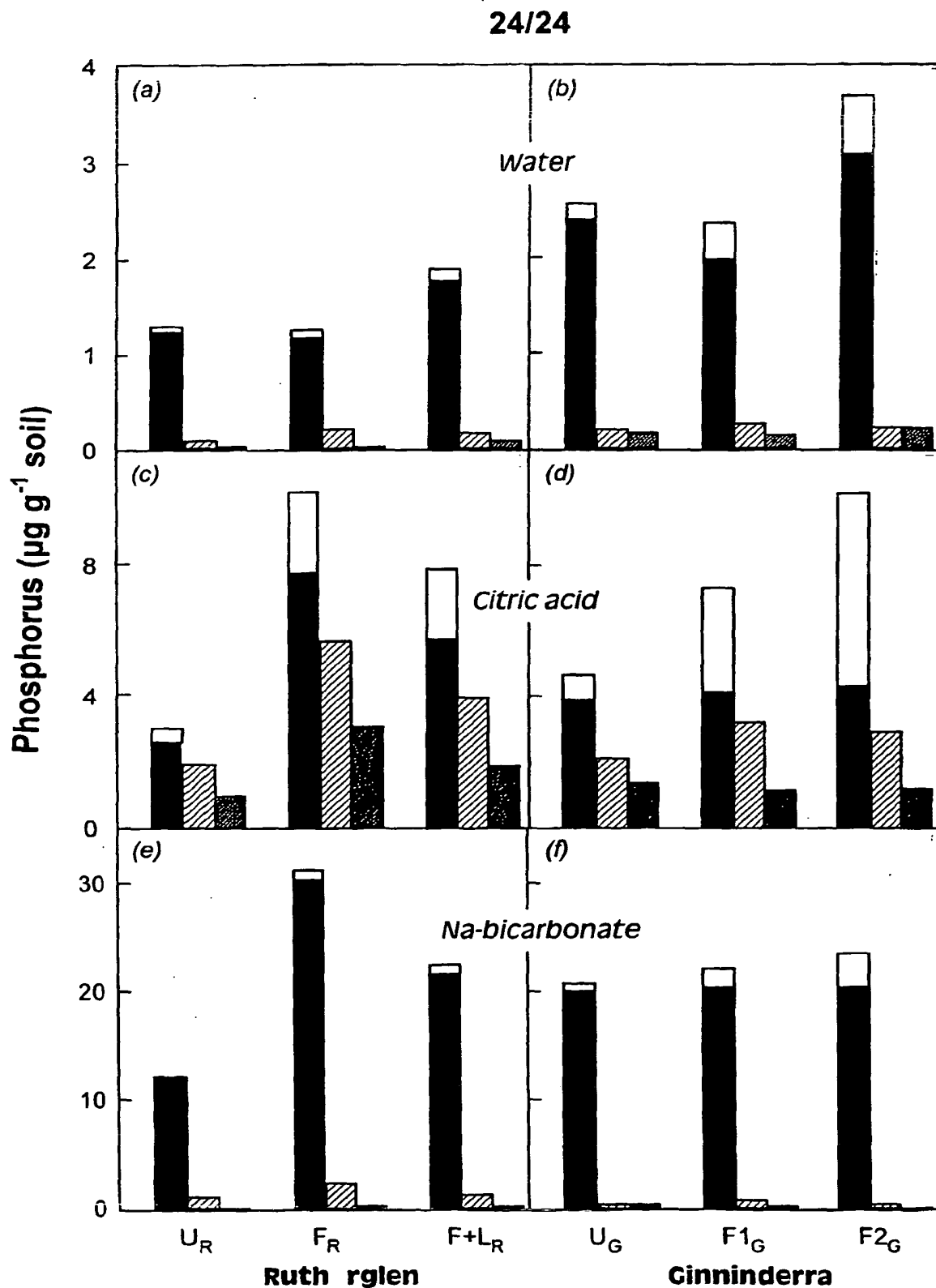


FIGURE 17